tred care and integration of the patient perspective in health care policy decisions. A major challenge for the integration of evidence on patient preference is that research on patient preferences is performed by various disciplines (e.g. psychology and economics) that do not share a common language. It has been recommended to perform conceptual and taxonomic work on the definition and conceptualisation of 'preference' and related terms. The aim of this study was to develop a taxonomy of preference-related terms. The taxonomy was developed in three steps: 1) the identification of preference-related terms; 2) providing all identified terms with a definition from the dictionary; and 3) the identification of dominant theories or models from (health) economics and psychology that deal with the reference-related terms. The proposed taxonomy consists of several building blocks that hold all identified preference-related terms and demonstrate the relation between terms. The building blocks are centred around a factual event. Ex ante to this factual event lies building block 1, "decision making" holding terms like "choice" and "decision". Ex post lie building block 2 "evaluation process" and building block 3 "outcome of evaluation process". Building block 3 holds terms like "utility", "quality of life" and "satisfaction". Building blocks 1-3 are influenced by building block 4 "the value system". This value system is divided in cognition, affect and conation and holds terms like "beliefs", "expectation", "attitudes", "desires" and "intention". In this taxonomy, preferences can be considered as a part of the value system. The proposed taxonomy is a first step towards conceptual clarity to facilitate the integration of research evidence in health care policy decisions.

PRM232

WHEN IT MAY NOT BE NECESSARY TO MODEL OVERALL SURVIVAL FOR ECONOMIC EVALUATIONS OF ANTI-CANCER DRUGS

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Overall survival (OS) is traditionally modelled in economic evaluations of anti-cancer drugs. However, OS is commonly associated with problems such as immaturity of the data, or confounding due to treatment switching or use of inappropriate treatments after progression. Fortunately, analysis of historical trials reveals that there is good evidence across a range of cancers that the mean time in post-progression survival (PPS) is equal between treatment arms, i.e. ΔPPS = 0. Therefore, we recommend that the default position is to assume equal mean times post-progression. If there is no a priori biological reason to suppose that the PPS times are likely to differ between treatments (e.g. due to differences in cross-resistance or long term toxicities between treatments), our recommendation is that it should be assumed that the mean time in progressive disease is equal between treatment arms if any of the following apply: OS is very immature; treatments post-progression are substantially imbalanced between treatment arms; in particular, treatment switching has occurred at progression; treatments post-progression are different to those routinely given in clinical practice; only single arm trials are available. If none of the above apply, or if there are a priorireasons to suggest that ΔPPS differs from 0, then the recommendation is to model OS and PFS in the traditional way. For chronic cancers, it is recommended that analyses should either assume equal times post initial treatment or equal time post progression. The assumption that ΔPPS = 0 substantially simplifies the economic analysis because cost-effectiveness becomes insensitive to OS. The methodology has been endorsed twice by NICE appraisal committees in assessments of drugs for chronic myeloid leukaemia. The cost-effectiveness of several drugs recently assessed by NICE are re-calculated using the methods proposed. Next, we give simplified formulae for the maximum drug price acceptable for reimbursement under the methodology.

PRM234

FEASIBILITY OF CONDUCTING RETROSPECTIVE STUDIES USING HASHTAGS AND SOCIAL MEDIA DATA FROM FACEBOOK AND TWITTER

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Various online services such as Socialbakers, Keyhole, Gnip offer tools to analyze, fetch and collect data from social media. This data is often presented in a form of interactive web based dashboards, displaying various trends: number of posts, mentions, shares, likes over time. Facebook and Twitter have an API to access data on social media profiles of real people. Users profiles usually have data on age, sex, employment and relationships status, specific group membership, etc. We conducted a simple feasibility study using Facebook API in diabetes area using profiles of people posting hashtags as a primary source of data. We then expanded the sample by adding people who liked, shared and reposted messages containing diabetes relaed hashtags #Diabetes, #dedoc, #ourD. We applied exclusion criteria to derive a sample consisting of patients only, hence targeting specific group of people. Our assumption was that people who interact with posts containing specific hashtag have diabetes. We used descriptive statistics to characterize obtained sample (n=17296) by calculating mean age, age distribution histogram, proportion of males and females and other descriptive metrics. We also calculated conditional probabilities of being in multiple disease area Facebook groups such as obesity groups or groups of people with increased risk of cardiovascular disease. Future area of research will be concentrated on aspects of in-degree centrality in network of diabetic people, hypothesis testing between two different groups, analyses of changes in positive/negative posting trends following drug launch, locating agents and influencers in the network and conducting prospective studies in social media using hashtags. Social Media data can be a valuable addition to a real life post launch data. Evidence on changes in positive/negative postings can be used as an additional piece of information in Phase IV studies or risk-sharing agreements.

PRM235

A FRAMEWORK FOR THE ECONOMIC EVALUATION OF SEQUENTIAL THERAPIES FOR CHRONIC CONDITIONS

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Cost-effectiveness models often require the consideration of a sequence of treatments. This enables the downstream implications of a treatment to be captured, and alternative sequences to be compared. However, when many treatments are available, the number of feasible sequences can be large. Also, if the objective is to maximise net benefit for a given ICER threshold, then a comparative analysis to identify the optimal sequence may not be possible. This is further compounded when using individual patient simulation (IPS), because of the increased computational burden compared with cohort approaches. The aim of this study was to undertake a systematic review of optimisation methods that are applicable to a treatment sequencing IPS model. 28 key papers were identified across a range of academic subjects. Metaheuristics including simulated annealing, tabu search and genetic algorithms have been applied to simulation-optimisation problems and a bespoke review framework was applied to determine their appropriateness. Based on the review, a framework for the economic evaluation of treatment sequences was developed. The framework considers the requirements of a cost-effectiveness model to efficiently evaluate sequences, the application of the reviewed metaheuristics to determine the optimal sequence, and the consideration of these results within a decision-making context. This will be applied to a case study in rheumatoid arthritis. Alternative metaheuristic algorithms will be applied in an attempt to estimate a (near) optimal treatment sequence. Preliminary results of these experiments will be available in time for the November 2014 ISPOR conference. If these methods prove successful and feasible, then the framework may have potential applicability to sequencing models in many diseases. Whether there is the capability for it to be applicable within the current process for decision-making organisations such as NICE remains an open question, however, identifying an optimal sequence in a decision problem is of interest to decision makers.

PRM236

NOVEL INDIRECT COMPARISON METHODOLOGY FOR ESTIMATING TIME-DEPENDENT RESPONSE TO ANTIMUSCARINICS FOR THE TREATMENT OF OAB

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BACKGROUND: Common indirect treatment comparison (ITC) methodology in overactive bladder involves combining absolute reduction in urge urinary incontinence (UUI) episodes at study endpoint (e.g., week 12) to estimate the overall treatment effect. Trials with differing endpoints must assume equivalence to be included in the network. Further, analyses of endpoint data are not sufficient to predict efficacy at intermediate time points (e.g. 4 or 6 weeks). We developed and tested an alternate methodology to utilize available intermediate time points into an ITC of published studies of fesoterodine and tolterodine. **METHODOLOGY:** Study-level mean UUI reduction over time can be represented as the percent reduction from baseline, which can be modeled as a monotonically-increasing function with a theoretical maximum of 100%. This function is expressed with two parameters: $\%red = b_i * time/(c_i + time)$, where b_i is the maximum possible reduction for treatment i, and c_i is the time required to reach half the maximum reduction. The inverse *%red* is a linear function of *1/time* that can be used within a Bayesian ITC framework to generate a placebo-adjusted indirect comparison of efficacy. **CONCLUSIONS:** The endpoint results obtained from the alternate methodology were comparable to those obtained from an endpoint ITC. This novel methodology has the additional advantage of utilizing all available time point data within a single analysis, which can then be used to generate efficacy estimates at intermediate time points, which may be utilized within economic models. Limitations include unavailability of uncertainty estimates of the *%red* variable and difficulty of estimating combinations of parameters within functional constraints. Finally, our alternate methodology may be used for any longitudinal data exhibiting a monotonic increase or decrease and may be expanded to include a network with multiple treatments.

PRM237

BAYESIAN MODELS FOR COST-EFFECTIVENESS ANALYSIS IN THE PRESENCE OF STRUCTURAL ZERO COSTS

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Bayesian modelling for cost-effectiveness data has received much attention in both the health economics and the statistical literature, in recent years. Cost-effectiveness data are characterised by a relatively complex structure of relationships linking a suitable measure of clinical benefit (\eg QALYs) and the associated costs. Simplifying assumptions, such as (bivariate) normality of the underlying distributions are usually not granted, particularly for the cost variable, which is characterised by markedly skewed distributions. In addition, individual-level datasets are often characterised by the presence of structural zeros in the cost variable. Hurdle models can be used to account for the presence of excess zeros in a distribution and have been applied in the context of cost data. We extend their application to cost-effectiveness data, defining a full Bayesian specification which consists of a pattern model for the individual probability of null costs, a marginal model for the costs and a conditional model for the measure of effectiveness (given the observed costs). The model is presented using a working example to describe its main features. In addition, we present a R package (BCEs0) that directly implements this framework and can be used to run a full Bayesian cost-effectiveness analysis of individual data in the presence of structural zero costs for some subjects.

PRM238

EFFECTIVE PRIORITISATION OF NATIONAL HEALTH TECHNOLOGY ASSESSMENTS

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Prioritisation of assessment topics is an essential activity within HTA. Failure to successfully identify technologies that are likely to have the greatest impact on the health system carries an opportunity cost that is measured in poorer decision